

0570
1017

#2

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/965,631

DATE: 10/18/2001

TIME: 09:53:30

Input Set : A:\LEX-0241-USA SEQLIST.txt

Output Set: N:\CRF3\10182001\I965631.raw

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4 <110> APPLICANT: Friddle, Carl Johan
5 Hilbun, Erin
7 <120> TITLE OF INVENTION: Novel Human Proteases and Polynucleotides Encoding the Same
9 <130> FILE REFERENCE: LEX-0241-USA
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/965,631
C--> 11 <141> CURRENT FILING DATE: 2001-09-27
11 <150> PRIOR APPLICATION NUMBER: US 60/236,689
12 <151> PRIOR FILING DATE: 2000-09-29
14 <160> NUMBER OF SEQ ID NOS: 7
16 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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19 <211> LENGTH: 966
20 <212> TYPE: DNA
21 <213> ORGANISM: homo sapiens
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26 tactggcggg gtcccgagga ctccggggat cagggactca tttttcagat cacagcattt 180
27 caggaggact tttacctaca cctgacgccg gatgctcagt tcttggctcc cgccttctcc 240
28 actgagcatc tgggcgtccc cctccagggg ctccaccggg gctcttcaga cctgcgacgc 300
29 tgcttctatt ctggggacgt gaacgcggag ccggactcgt tcgctgctgt gagcctgtgc 360
30 ggggggctcc gcggagcctt tggctaccga ggcgcggagt atgtcattag cccgctgccc 420
31 aatgctagcg cgcggcgggc gcagcgcaac agccaggggc cacaccttct ccagcgccgg 480
32 ggtgttccgg gcgggccttc cggagacccc acctctcgct gcggggtggc ctccgggctg 540
33 aaccccgcca tcctacgggc cctggaccct tacaagccgc ggccggcggg cttcggggag 600
34 agtcgtagcc ggcgcaggtc tgggcgcgcc aagcgtttcg tgtctatccc gcggtacgtg 660
35 gagacgctgg tggtcgcgga cgagtcaatg gtcaagttcc acggcgcgga cctggaacat 720
36 tatctgctga cgtgctggc aacggcgggc cgactctacc gccatcccag catcctcaac 780
37 cccatcaaca tcgttgtggt caaggtgctg cttcttagag atcgtgactc cgggcccagg 840
38 gtcaccggca atgcggccct gacgctgcgc aacttctgtg cctggcagaa gaagctgaac 900
39 aaagtgaagt acaagcaccc cgagtactgg gacactgcca tcctcttcac caggcaggag 960
40 agttga 966
42 <210> SEQ ID NO: 2
43 <211> LENGTH: 321
44 <212> TYPE: PRT
45 <213> ORGANISM: homo sapiens
47 <400> SEQUENCE: 2
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49 1 5 10 15
50 Gly Gly Ser Glu Pro Glu Arg Glu Val Val Val Pro Ile Arg Leu Asp
51 20 25 30
52 Pro Asp Ile Asn Gly Arg Arg Tyr Tyr Trp Arg Gly Pro Glu Asp Ser
53 35 40 45
54 Gly Asp Gln Gly Leu Ile Phe Gln Ile Thr Ala Phe Gln Glu Asp Phe
55 50 55 60
56 Tyr Leu His Leu Thr Pro Asp Ala Gln Phe Leu Ala Pro Ala Phe Ser
57 65 70 75 80
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58 Thr Glu His Leu Gly Val Pro Leu Gln Gly Leu Thr Gly Gly Ser Ser
59           85           90           95
60 Asp Leu Arg Arg Cys Phe Tyr Ser Gly Asp Val Asn Ala Glu Pro Asp
61           100           105           110
62 Ser Phe Ala Ala Val Ser Leu Cys Gly Gly Leu Arg Gly Ala Phe Gly
63           115           120           125
64 Tyr Arg Gly Ala Glu Tyr Val Ile Ser Pro Leu Pro Asn Ala Ser Ala
65           130           135           140
66 Pro Ala Ala Gln Arg Asn Ser Gln Gly Ala His Leu Leu Gln Arg Arg
67 145           150           155           160
68 Gly Val Pro Gly Gly Pro Ser Gly Asp Pro Thr Ser Arg Cys Gly Val
69           165           170           175
70 Ala Ser Gly Trp Asn Pro Ala Ile Leu Arg Ala Leu Asp Pro Tyr Lys
71           180           185           190
72 Pro Arg Arg Ala Gly Phe Gly Glu Ser Arg Ser Arg Arg Arg Ser Gly
73           195           200           205
74 Arg Ala Lys Arg Phe Val Ser Ile Pro Arg Tyr Val Glu Thr Leu Val
75           210           215           220
76 Val Ala Asp Glu Ser Met Val Lys Phe His Gly Ala Asp Leu Glu His
77 225           230           235           240
78 Tyr Leu Leu Thr Leu Ala Thr Ala Ala Arg Leu Tyr Arg His Pro
79           245           250           255
80 Ser Ile Leu Asn Pro Ile Asn Ile Val Val Val Lys Val Leu Leu Leu
81           260           265           270
82 Arg Asp Arg Asp Ser Gly Pro Lys Val Thr Gly Asn Ala Ala Leu Thr
83           275           280           285
84 Leu Arg Asn Phe Cys Ala Trp Gln Lys Lys Leu Asn Lys Val Ser Asp
85           290           295           300
86 Lys His Pro Glu Tyr Trp Asp Thr Ala Ile Leu Phe Thr Arg Gln Glu
87 305           310           315           320
88 Ser
91 <210> SEQ ID NO: 3
92 <211> LENGTH: 2853
93 <212> TYPE: DNA
94 <213> ORGANISM: homo sapiens
96 <400> SEQUENCE: 3
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98 ccagagcggg aggtagtcgt tcccatccga ctggaccggg acattaacgg ccgccgctac      120
99 tactggcggg gtcccgagga ctccggggat cagggactca tttttcagat cacagcattt      180
100 caggaggact ttacctaca cctgacgccg gatgctcagt tcttggctcc cgccttctcc      240
101 actgagcatt tgggcgtccc cctccagggg ctccacgggg gctcttcaga cctgcgacgc      300
102 tgcttctatt ctggggacgt gaacgccgag ccggactcgt tcgctgctgt gagcctgtgc      360
103 ggggggctcc gcggagcctt tggctaccga ggcgcggagt atgtcattag cccgctgccc      420
104 aatgctagcg cgccggcggc gcagcgcaac agccagggcg cacaccttct ccagcgccgg      480
105 ggtgttccgg gcgggccttc cggagacccc acctctcgct gcggggtggc ctcgggctgg      540
106 aaccccgcca tcctacgggc cctggaccct tacaagccgc ggcgggcggg cttcggggag      600
107 agtcgtagcc ggcgcaggtc tgggcgcgcc aagcgtttcg tgtctatccc gcggtacgtg      660
108 gagacgctgg tggtcgcgga cgagtcaatg gtcaagtccc acggcgcgga cctggaacat      720
109 tatctgctga cgctgctggc aacggcgggc cgactctacc gccatcccag catcctcaac      780

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110 cccatcaaca tcgttggtg caaggtgctg cttcttagag atcgtgactc cgggccaag      840
111 gtcaccggca atgcggccct gacgctgcgc aacttctgtg cctggcagaa gaagctgaac      900
112 aaagtgagtg acaagcacc cagagtactg gacactgcc tctcttcac caggcaggac      960
113 ctgtgtggag ccaccacctg tgacacctg ggcattggctg atgtgggtac catgtgtgac     1020
114 cccaagagaa gctgctctgt cattgaggac gatgggcttc catcagcctt caccactgcc     1080
115 cagagctgg gccacgtgtt caacatgcc catgacaatg tgaaagtctg tgaggaggtg     1140
116 tttgggaagc tccgagccaa ccacatgatg tccccgacct tcatccagat cgaccgtgcc     1200
117 aacccttgt cagcctgcag tgctgccatc atcaccgact tctggacag cgggcacggt     1260
118 gactgcctcc tggaccaacc cagcaagccc atctccctgc ccgaggatct gccgggcgcc     1320
119 agctacacc tgagccagca gtgcgagctg gcttttggcg tgggctccaa gccctgtcct     1380
120 tacatgcagt actgcacca gctgtgtgtc accgggaagg ccaagggaca gatggtgtgc     1440
121 cagaccgcc acttcccctg ggccgatgtg accagctgtg gcgagggcaa gctctgcctc     1500
122 aaaggggct gcgtggagag acacaacctc aacaagcaca ggggtggatg ttcctgggcc     1560
123 aaatgggatc cctatggccc ctgctgcgcg acatgtggtg ggggcgtgca gctggccagg     1620
124 aggcagtga ccaacccca cctgccaac gggggcaagt actgcgagg agtgagggtg     1680
125 aaataccgat cctgcaatct ggagccctgc cccagctcag cctccggaaa gagcttccgg     1740
126 gaggagcagt gtgaggcttt caacggctac aaccacagca ccaaccggct cactctcgcc     1800
127 gtggcatggg tgcccaagta ctccggcgtg tctccccggg acaagtgcaa gctcatctgc     1860
128 cgagccaatg gactggcta cttctatgtg ctggcaccca aggtggtgga cggcacgctg     1920
129 tgctctcctg actccacctc cgtctgtgtc caaggcaagt gcatcaaggc tggctgtgat     1980
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132 gccatcccc cagcgccctc aagcatcgac atccgccagc gcggttacia agggctgac     2160
133 ggggatgaca actacctggc tctgaagaac agccaaggca agtacctgct caacgggcat     2220
134 ttcgtggtgt cggcggtgga gcgggacctg gtggtgaagg gcagtctgct gcggtacagc     2280
135 ggcacgggca cagcggtgga gacgctgcag gcttcccggc ccatactgga gccgctgacc     2340
136 gtggagggtc tctccgtggg gaagatgaca ccgccccggg tccgctactc cttctatctg     2400
137 cccaagagc ctcgggagga caagtcctct catcccaagg acccccgggg accctctgtc     2460
138 ttgcacaaca gcgtcctcag cctctccaac caggtggagc agccggacga caggccccct     2520
139 gcacgctggg tggtggcag ctgggggccc tgctccgcga gctgcggcag tggcctgcag     2580
140 aagcggggcg tggactgtcg gggctccgcc gggcagcgca cggtccctgc ctgtgatgca     2640
141 gccatcggc ccgtggagac acaagcctgc ggggagccct gccccacctg ggagctcagc     2700
142 gcctggtcac cctgtcccaa gagctgcggc cggggatttc agaggcgctc actcaagtgt     2760
143 gtggggccac gaggcgggct gctggcccgg gaccagtga acttgaccg caagccccag     2820
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146 <210> SEQ ID NO: 4

147 <211> LENGTH: 950

148 <212> TYPE: PRT

149 <213> ORGANISM: homo sapiens

151 <400> SEQUENCE: 4

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154 Gly Gly Ser Glu Pro Glu Arg Glu Val Val Val Pro Ile Arg Leu Asp

155 20 25 30

156 Pro Asp Ile Asn Gly Arg Arg Tyr Trp Arg Gly Pro Glu Asp Ser

157 35 40 45

158 Gly Asp Gln Gly Leu Ile Phe Gln Ile Thr Ala Phe Gln Glu Asp Phe

159 50 55 60

160 Tyr Leu His Leu Thr Pro Asp Ala Gln Phe Leu Ala Pro Ala Phe Ser

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161 65              70              75              80
162 Thr Glu His Leu Gly Val Pro Leu Gln Gly Leu Thr Gly Gly Ser Ser
163              85              90              95
164 Asp Leu Arg Arg Cys Phe Tyr Ser Gly Asp Val Asn Ala Glu Pro Asp
165              100             105             110
166 Ser Phe Ala Ala Val Ser Leu Cys Gly Gly Leu Arg Gly Ala Phe Gly
167              115             120             125
168 Tyr Arg Gly Ala Glu Tyr Val Ile Ser Pro Leu Pro Asn Ala Ser Ala
169              130             135             140
170 Pro Ala Ala Gln Arg Asn Ser Gln Gly Ala His Leu Leu Gln Arg Arg
171 145             150             155             160
172 Gly Val Pro Gly Gly Pro Ser Gly Asp Pro Thr Ser Arg Cys Gly Val
173              165             170             175
174 Ala Ser Gly Trp Asn Pro Ala Ile Leu Arg Ala Leu Asp Pro Tyr Lys
175              180             185             190
176 Pro Arg Arg Ala Gly Phe Gly Glu Ser Arg Ser Arg Arg Arg Ser Gly
177              195             200             205
178 Arg Ala Lys Arg Phe Val Ser Ile Pro Arg Tyr Val Glu Thr Leu Val
179              210             215             220
180 Val Ala Asp Glu Ser Met Val Lys Phe His Gly Ala Asp Leu Glu His
181 225             230             235             240
182 Tyr Leu Leu Thr Leu Leu Ala Thr Ala Ala Arg Leu Tyr Arg His Pro
183              245             250             255
184 Ser Ile Leu Asn Pro Ile Asn Ile Val Val Val Lys Val Leu Leu Leu
185              260             265             270
186 Arg Asp Arg Asp Ser Gly Pro Lys Val Thr Gly Asn Ala Ala Leu Thr
187              275             280             285
188 Leu Arg Asn Phe Cys Ala Trp Gln Lys Lys Leu Asn Lys Val Ser Asp
189              290             295             300
190 Lys His Pro Glu Tyr Trp Asp Thr Ala Ile Leu Phe Thr Arg Gln Asp
191 305             310             315             320
192 Leu Cys Gly Ala Thr Thr Cys Asp Thr Leu Gly Met Ala Asp Val Gly
193              325             330             335
194 Thr Met Cys Asp Pro Lys Arg Ser Cys Ser Val Ile Glu Asp Asp Gly
195              340             345             350
196 Leu Pro Ser Ala Phe Thr Thr Ala His Glu Leu Gly His Val Phe Asn
197              355             360             365
198 Met Pro His Asp Asn Val Lys Val Cys Glu Glu Val Phe Gly Lys Leu
199              370             375             380
200 Arg Ala Asn His Met Met Ser Pro Thr Leu Ile Gln Ile Asp Arg Ala
201 385             390             395             400
202 Asn Pro Trp Ser Ala Cys Ser Ala Ala Ile Ile Thr Asp Phe Leu Asp
203              405             410             415
204 Ser Gly His Gly Asp Cys Leu Leu Asp Gln Pro Ser Lys Pro Ile Ser
205              420             425             430
206 Leu Pro Glu Asp Leu Pro Gly Ala Ser Tyr Thr Leu Ser Gln Gln Cys
207              435             440             445
208 Glu Leu Ala Phe Gly Val Gly Ser Lys Pro Cys Pro Tyr Met Gln Tyr
209              450             455             460

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210 Cys Thr Lys Leu Trp Cys Thr Gly Lys Ala Lys Gly Gln Met Val Cys
211 465 470 475 480
212 Gln Thr Arg His Phe Pro Trp Ala Asp Gly Thr Ser Cys Gly Glu Gly
213 485 490 495
214 Lys Leu Cys Leu Lys Gly Ala Cys Val Glu Arg His Asn Leu Asn Lys
215 500 505 510
216 His Arg Val Asp Gly Ser Trp Ala Lys Trp Asp Pro Tyr Gly Pro Cys
217 515 520 525
218 Ser Arg Thr Cys Gly Gly Gly Val Gln Leu Ala Arg Arg Gln Cys Thr
219 530 535 540
220 Asn Pro Thr Pro Ala Asn Gly Gly Lys Tyr Cys Glu Gly Val Arg Val
221 545 550 555 560
222 Lys Tyr Arg Ser Cys Asn Leu Glu Pro Cys Pro Ser Ser Ala Ser Gly
223 565 570 575
224 Lys Ser Phe Arg Glu Glu Gln Cys Glu Ala Phe Asn Gly Tyr Asn His
225 580 585 590
226 Ser Thr Asn Arg Leu Thr Leu Ala Val Ala Trp Val Pro Lys Tyr Ser
227 595 600 605
228 Gly Val Ser Pro Arg Asp Lys Cys Lys Leu Ile Cys Arg Ala Asn Gly
229 610 615 620
230 Thr Gly Tyr Phe Tyr Val Leu Ala Pro Lys Val Val Asp Gly Thr Leu
231 625 630 635 640
232 Cys Ser Pro Asp Ser Thr Ser Val Cys Val Gln Gly Lys Cys Ile Lys
233 645 650 655
234 Ala Gly Cys Asp Gly Asn Leu Gly Ser Lys Lys Arg Phe Asp Lys Cys
235 660 665 670
236 Gly Val Cys Gly Gly Asp Asn Lys Ser Cys Lys Lys Val Thr Gly Leu
237 675 680 685
238 Phe Thr Lys Pro Met His Gly Tyr Asn Phe Val Val Ala Ile Pro Ala
239 690 695 700
240 Gly Ala Ser Ser Ile Asp Ile Arg Gln Arg Gly Tyr Lys Gly Leu Ile
241 705 710 715 720
242 Gly Asp Asp Asn Tyr Leu Ala Leu Lys Asn Ser Gln Gly Lys Tyr Leu
243 725 730 735
244 Leu Asn Gly His Phe Val Val Ser Ala Val Glu Arg Asp Leu Val Val
245 740 745 750
246 Lys Gly Ser Leu Leu Arg Tyr Ser Gly Thr Gly Thr Ala Val Glu Ser
247 755 760 765
248 Leu Gln Ala Ser Arg Pro Ile Leu Glu Pro Leu Thr Val Glu Val Leu
249 770 775 780
250 Ser Val Gly Lys Met Thr Pro Pro Arg Val Arg Tyr Ser Phe Tyr Leu
251 785 790 795 800
252 Pro Lys Glu Pro Arg Glu Asp Lys Ser Ser His Pro Lys Asp Pro Arg
253 805 810 815
254 Gly Pro Ser Val Leu His Asn Ser Val Leu Ser Leu Ser Asn Gln Val
255 820 825 830
256 Glu Gln Pro Asp Asp Arg Pro Pro Ala Arg Trp Val Ala Gly Ser Trp
257 835 840 845
258 Gly Pro Cys Ser Ala Ser Cys Gly Ser Gly Leu Gln Lys Arg Ala Val

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VERIFICATION SUMMARY

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Input Set : A:\LEX-0241-USA SEQLIST.txt

Output Set: N:\CRF3\10182001\I965631.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date